

DNA SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 09:08:28 ; Search time 4212 Seconds
(without alignments)
10959.243 Million cell updates/sec

Title: US-10-061-043A-34
Perfect score: 1065
Sequence: 1 atgccattcctcgggcagga.....ttatcaactgttcaagttc 1065

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

Searched SEQ 34 in DNA
databases

Also searched DNA using SEQ 35(PRT)
← oligomer search w/ SEQ 34

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						FD 8/9/01	
						FD 2/1/01	
						JP-R 2/1/01	
Result No.	Score	% Match	Query Length	DB	ID	Description	
1	1065	100.0	1065	6	BD097188	40 0157203	BD097188 Novel gen
2	1065	100.0	1068	9	AY059629	11/2001	AY059629 Homo sapi
3	1065	100.0	1391	9	HSA420108	11/2001	AJ420108 Homo sapi
4	1065	100.0	1491	6	BD097189		BD097189 Novel gen
5	1065	100.0	1506	6	AX714560	EP 1293567 3/17/03	AX714560 Sequence
6	1065	100.0	1506	9	AK056986	10/2001	AK056986 Homo sapi
P-7	1065	100.0	1507	6	BD276548		BD276548 FULL-LENG
P-8	1065	100.0	1507	6	AX048112		AX048112 Sequence
9	1013	95.1	2584	6	AX780555	40 03039443 5/15/03	AX780555 Sequence
10	914.6	85.9	1967	10	BC027211	4/4/02	BC027211 Mus muscu
11	914.6	85.9	2064	10	AF441120	12/2001	AF441120 Mus muscu
12	873	82.0	1053	10	AY059628	11/2001	AY059628 Rattus no
13	784.8	73.7	1212	9	BC024030	2002	BC024030 Homo sapi
P 14	649.4	61.0	828	6	AR339520		AR339520 Sequence
15	569.4	53.5	1804	5	BC052112	2002	BC052112 Danio rer
16	468.2	44.0	2008	10	BC014749		BC014749 Mus muscu
17	450.4	42.3	1991	5	AY398345		AY398345 Danio rer
18	427.2	40.1	1327	9	AB070270		AB070270 Homo sapi
19	427.2	40.1	1611	9	AF419858		AF419858 Homo sapi
20	392.8	36.9	2382	9	BC050393		BC050393 Homo sapi
21	372.6	35.0	1303	9	BC012143		BC012143 Homo sapi
22	372.6	35.0	1303	9	BC020249		BC020249 Homo sapi
23	366.2	34.4	819	9	AF174605		AF174605 Homo sapi
24	296	27.8	338	6	AX779162		AX779162 Sequence
25	288.4	27.1	934	9	BC035555		BC035555 Homo sapi
c 26	228.2	21.4	541	6	AX283893		AX283893 Sequence
c 27	228.2	21.4	714	6	AX283892		AX283892 Sequence
c 28	188.8	17.7	54210	9	AC127544		AC127544 Homo sapi
29	188.8	17.7	167919	9	AC090193		AC090193 Homo sapi
c 30	188.8	17.7	167955	9	AF267170		AF267170 Homo sapi
c 31	188.8	17.7	202142	9	AF254981		AF254981 Homo sapi
c 32	188	17.7	72533	2	AC127543		AC127543 Homo sapi
c 33	164.2	15.4	228212	2	AC103138		AC103138 Rattus no

OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 09:05:58 ; Search time 465 Seconds
(without alignments)
9729.744 Million cell updates/sec

Title: US-10-061-043A-34
Perfect score: 1065
Sequence: 1 atgccattcctcgggcagga.....ttatcaacttggtcaagttc 1065

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1065	100.0	1065	4	AAH43090 <i>WO 01 57203</i> Aah43090 Nucleotid
2	1065	100.0	1065	6	ABQ79511 <i>Applicant's WO</i> Abq79511 Human MAF
3	1065	100.0	1491	4	AAH43099 Aah43099 Nucleotid
4	1065	100.0	1506	6	ABX04205 <i>3/2001</i> Abx04205 Human mRNA
5	1065	100.0	1506	7	ADA53676 <i>7/2001</i> Ada53676 Human cod
6	1065	100.0	1507	5	AAC88120 <i>WO 0070047</i> Aac88120 Human FLE
7	1033.4	97.0	1035	6	ABQ79509 <i>Appl.</i> Abq79509 Human MAF
<i>p</i> 8	961	90.2	2067	9	ADE24728 <i>US 2003 077 288</i> Ade24728 Mouse cDN

Chinese
 Priority to 8/23/00
 ↑ Published 3/13/02

	9	922.4	86.6	1804	6	ABN86757	CN1339455	Abn86757	Eukaryoti
	10	873	82.0	1050	6	ABQ79508	Appl.	Abq79508	Rat MAFBX
	11	868.6	81.6	1302	3	AAF15631	WO 2000 55174	Aaf15631	Human pro
	12	649.4	61.0	828	4	AAI59118		Aai59118	Human pol
	13	649.4	61.0	828	8	ADB49101		Adb49101	Novel hum
	14	644.6	60.5	806	4	AAI60904		Aai60904	Human pol
	15	553.8	52.0	570	7	ABZ20098		Abz20098	Group III
c	16	427.2	40.1	1967	4	AAI61180		Aai61180	Human pol
	17	427.2	40.1	2431	4	AAI59394		Aai59394	Human pol
	18	388.4	36.5	2230	3	AAC76579		Aac76579	Human ORF
	19	371	34.8	876	6	ABS51579		Abs51579	Human cDN
	20	369.2	34.7	462	8	ACH26226		Ach26226	Human adu
	21	366.2	34.4	1214	3	AAZ93368		Aaz93368	Sequence
	22	366.2	34.4	1214	6	AAL41059		Aal41059	cDNA of H
	23	357.4	33.6	1285	4	ABK41870		Abk41870	cDNA enco
	24	357.4	33.6	1285	8	ADB59537		Adb59537	Connectiv
	25	272.4	25.6	1142	5	AAS75702		Aas75702	DNA encod
	26	229	21.5	382	2	AAT23657		Aat23657	Human gen
c	27	228.2	21.4	541	6	AAS62039		Aas62039	Porcine m
c	28	228.2	21.4	714	6	AAS62038		Aas62038	Porcine m
	29	210.8	19.8	578	6	ABX04143		Abx04143	Human cDN
	30	149.2	14.0	293	7	ABX88862		Abx88862	Corn ear-
	31	134.8	12.7	492	8	ACH16421		Ach16421	Human adu
	32	116.8	11.0	315	2	AAV88660		Aav88660	EST clone
	33	107.8	10.1	2961	6	ABK35777		Abk35777	cDNA sequ
	34	107.8	10.1	2991	2	AAX99860		Aax99860	Human sec
	35	107.8	10.1	2991	4	AAS59284		Aas59284	Human cDN
	36	107.8	10.1	2991	6	ABA90953		Aba90953	Human pol
c	37	105.6	9.9	224	7	ABZ19178		Abz19178	Group III
c	38	105.6	9.9	224	7	ABZ19937		Abz19937	Group III
	39	105.6	9.9	224	7	ABZ19700		Abz19700	Group III
c	40	105.6	9.9	224	7	ABZ19066		Abz19066	Group III
c	41	105.6	9.9	224	7	ABZ19773		Abz19773	Group III
c	42	105.6	9.9	224	7	ABZ19978		Abz19978	Group III
c	43	105.6	9.9	224	7	ABZ19160		Abz19160	Group III
c	44	105.6	9.9	224	7	ABZ19307		Abz19307	Group III
c	45	105.6	9.9	224	7	ABZ19505		Abz19505	Group III

ALIGNMENTS

RESULT 1

AAH43090

ID AAH43090 standard; DNA; 1065 BP.

XX

AC AAH43090;

XX

DT 15-OCT-2001 (first entry)

XX

DE Nucleotide sequence of a human tig104-alpha protein.

XX

KW Human; tig104-alpha; proteasome; proteolysis-controlling factor; tumour;

KW leukemia; lung cancer; stomach cancer; heart muscle; skeletal muscle;

KW muscle differentiation; myocardial infarction; cancer; ss.

XX

OS Homo sapiens.

OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 11:12:09 ; Search time 109 Seconds
 (without alignments)
 5422.227 Million cell updates/sec

Title: US-10-061-043A-34
 Perfect score: 1065
 Sequence: 1 atgccattcctcgggcagga.....ttatcaacttggtcaagttc 1065

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query	Length	DB	ID	Description
	No.	Score					
c c	1	649.4	61.0	828	4	US-09-620-312D-1011	Sequence 1011, Ap
	2	149.2	14.0	293	4	US-09-313-294A-7322	Sequence 7322, Ap
	3	49.2	4.6	7218	1	US-08-232-463-14	Sequence 14, Appl
	4	42.4	4.0	894	4	US-09-252-991A-9692	Sequence 9692, Ap
	5	42.4	4.0	2658	4	US-09-252-991A-9558	Sequence 9558, Ap
	6	42.4	4.0	2799	4	US-09-252-991A-9604	Sequence 9604, Ap
	7	39	3.7	2742	3	US-08-911-853-16	Sequence 16, Appl
	8	39	3.7	2742	3	US-09-479-409-16	Sequence 16, Appl
	9	39	3.7	2742	4	US-09-479-453-16	Sequence 16, Appl
	10	39	3.7	17612	3	US-08-911-853-29	Sequence 29, Appl
	11	39	3.7	17612	3	US-09-479-409-29	Sequence 29, Appl
	12	39	3.7	17612	4	US-09-479-453-29	Sequence 29, Appl

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 13:11:10 ; Search time 444 Seconds
(without alignments)
8399.215 Million cell updates/sec

Title: US-10-061-043A-34
Perfect score: 1065
Sequence: 1 atgccattcctcgggcagga.....ttatcaacttggtcaagttc 1065

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1065	100.0	1065	14	US-10-061-043A-34 <i>Appl.</i>	Sequence 34, Appl
2	1065	100.0	1065	15	US-10-060-634C-34 <i>related</i>	Sequence 34, Appl
3	1065	100.0	1506	14	US-10-096-534-64 <i>3/12/01</i>	Sequence 64, Appl
4	1065	100.0	1506	15	US-10-094-749-1244 <i>9/14/01</i>	Sequence 1244, Ap
5	1033.4	97.0	1035	14	US-10-061-043A-26 <i>Appl.</i>	Sequence 26, Appl
6	1033.4	97.0	1035	15	US-10-060-634C-26 <i>related</i>	Sequence 26, Appl
7	961	90.2	2067	14	✓US-10-050-686A-1 <i>US20030077288</i>	Sequence 1, Appli
8	873	82.0	1050	14	US-10-061-043A-24 <i>Appl.</i>	Sequence 24, Appl
9	873	82.0	1050	15	US-10-060-634C-24 <i>related</i>	Sequence 24, Appl
10	868.6	81.6	1302	9	✓US-09-925-300-66	Sequence 66, Appl
11	649.4	61.0	828	14	US-10-037-270-1011	Sequence 1011, Ap
12	649.4	61.0	828	15	US-10-117-722-1011	Sequence 1011, Ap
13	371	34.8	876	14	US-10-043-487-159	Sequence 159, App
14	369.2	34.7	462	10	US-09-918-995-13438	Sequence 13438, A
15	366.2	34.4	1214	13	US-10-042-417-45	Sequence 45, Appl
16	357.4	33.6	1285	9	US-09-764-847-268	Sequence 268, App
17	357.4	33.6	1285	14	US-10-092-154-268	Sequence 268, App
18	281	26.4	425	15	US-10-242-535A-23658	Sequence 23658, A
c 19	228.2	21.4	541	14	US-10-257-826A-165	Sequence 165, App
c 20	228.2	21.4	714	14	US-10-257-826A-164	Sequence 164, App
21	210.8	19.8	578	14	US-10-096-534-1	Sequence 1, Appli
c 22	163.2	15.3	814	15	US-10-027-632-149506	Sequence 149506,
c 23	163.2	15.3	814	15	US-10-027-632-149507	Sequence 149507,
24	134.8	12.7	492	10	US-09-918-995-3633	Sequence 3633, Ap
25	116.8	11.0	315	13	US-10-040-739-1138	Sequence 1138, Ap
26	107.8	10.1	2961	10	US-09-822-846-168	Sequence 168, App
27	107.8	10.1	2991	9	US-09-729-674-155	Sequence 155, App
28	62	5.8	483	15	US-10-242-535A-40062	Sequence 40062, A
c 29	60.8	5.7	390	14	US-10-060-036-2936	Sequence 2936, Ap
30	49.2	4.6	569	9	US-09-764-860-299	Sequence 299, App
31	49.2	4.6	569	9	US-09-764-904-40	Sequence 40, Appl
32	49.2	4.6	569	14	US-10-091-548-40	Sequence 40, Appl
33	49.2	4.6	569	14	US-10-074-095-299	Sequence 299, App
34	49.2	4.6	569	15	US-10-212-872-299	Sequence 299, App
35	43.4	4.1	4176	15	US-10-439-703-16	Sequence 16, Appl
36	42.4	4.0	2022	12	US-10-282-122A-31503	Sequence 31503, A
37	40.6	3.8	2332	9	US-09-764-860-1197	Sequence 1197, Ap
38	40.6	3.8	2332	9	US-09-764-904-136	Sequence 136, App
39	40.6	3.8	2332	14	US-10-091-548-136	Sequence 136, App
40	40.6	3.8	2332	14	US-10-074-095-1197	Sequence 1197, Ap
41	40.6	3.8	2332	15	US-10-212-872-1197	Sequence 1197, Ap
42	40.4	3.8	423	15	US-10-260-238-4714	Sequence 4714, Ap
43	39.6	3.7	1242	12	US-10-282-122A-25883	Sequence 25883, A
44	39.2	3.7	1476	15	US-10-369-493-32472	Sequence 32472, A
45	39.2	3.7	2934	10	US-09-938-901-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-061-043A-34

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 11:10:24 ; Search time 2716 Seconds
(without alignments)
11709.581 Million cell updates/sec

Title: US-10-061-043A-34
Perfect score: 1065
Sequence: 1 atgccattcctcgggcagga.....ttatcaacttggtcaagttc 1065

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	949	89.1	952	29	AY409554	AY409554 Homo sapi
	2	914.6	85.9	1955	11	AK014612	AK014612 Mus muscu
	3	914.6	85.9	2719	11	AK014793	AK014793 Mus muscu
	4	813	76.3	952	29	AY409556	AY409556 Mus muscu
	5	804	75.5	948	29	AY409555	AY409555 Pan trogl
	6	795.4	74.7	811	12	BM715687	BM715687 UI-E-EJ0-
	7	790.6	74.2	836	13	BU177535	BU177535 AGENCOURT
	8	699	65.6	722	12	BM715409	BM715409 UI-E-CL1-
	9	688.6	64.7	886	13	BX417886	BX417886 BX417886
c	10	666.6	62.6	1178	13	BX338528	BX338528 BX338528
	11	628	59.0	941	13	BU519820	BU519820 AGENCOURT
	12	602	56.5	757	12	BG722480	BG722480 602693725
	13	592	55.6	678	14	CB446966	CB446966 700945 MA
	14	580	54.5	772	12	BI659576	BI659576 603303129
	15	572	53.7	572	14	CB157454	CB157454 K-EST0216
	16	570.4	53.6	733	12	BI854478	BI854478 603380158
	17	563.6	52.9	650	14	CF367478	CF367478 842229 MA
	18	560.4	52.6	573	14	CB118722	CB118722 K-EST0165
	19	555.2	52.1	1036	12	BM544031	BM544031 AGENCOURT
	20	545.6	51.2	973	13	BQ933838	BQ933838 AGENCOURT
c	21	541.4	50.8	761	12	BI084995	BI084995 602869693
	22	536	50.3	715	13	BX103026	BX103026 BX103026
	23	533.6	50.1	1104	10	BF583907	BF583907 602096914
	24	531.6	49.9	557	10	AW957248	AW957248 EST369318
	25	528.4	49.6	979	13	BQ930818	BQ930818 AGENCOURT
	26	514.4	48.3	685	12	BG722256	BG722256 602693426
	27	506.8	47.6	776	12	BI459158	BI459158 603199342
	28	500.2	47.0	561	10	BF193342	BF193342 244886 MA
	29	484.4	45.5	781	13	BU469022	BU469022 603363560
	30	478.8	45.0	538	9	AA033704	AA033704 zf01d10.s
c	31	478	44.9	507	10	BE077170	BE077170 RC5-BT060
	32	476.8	44.8	512	10	AW464353	AW464353 BP230015B
	33	475	44.6	667	12	BM763083	BM763083 K-EST0044
	34	473	44.4	491	10	AW956133	AW956133 EST368203
	35	468.2	44.0	2009	11	AK018626	AK018626 Mus muscu
	36	467	43.8	537	10	BE751158	BE751158 202904 MA
	37	466.6	43.8	2002	11	AK008027	AK008027 Mus muscu
c	38	465.6	43.7	892	13	BX371779	BX371779 BX371779
c	39	465.6	43.7	895	13	BX371780	BX371780 BX371780
c	40	464.4	43.6	764	14	CA503406	CA503406 UI-CF-FN0
	41	455.6	42.8	786	9	AU080359	AU080359 AU080359
	42	451.4	42.4	453	13	BX500665	BX500665 DKFZp779B
	43	438	41.1	600	14	CA528567	CA528567 8081-27 M
	44	433.4	40.7	747	12	BI654311	BI654311 603280259
	45	428.4	40.2	443	12	BM703879	BM703879 UI-E-CL1-